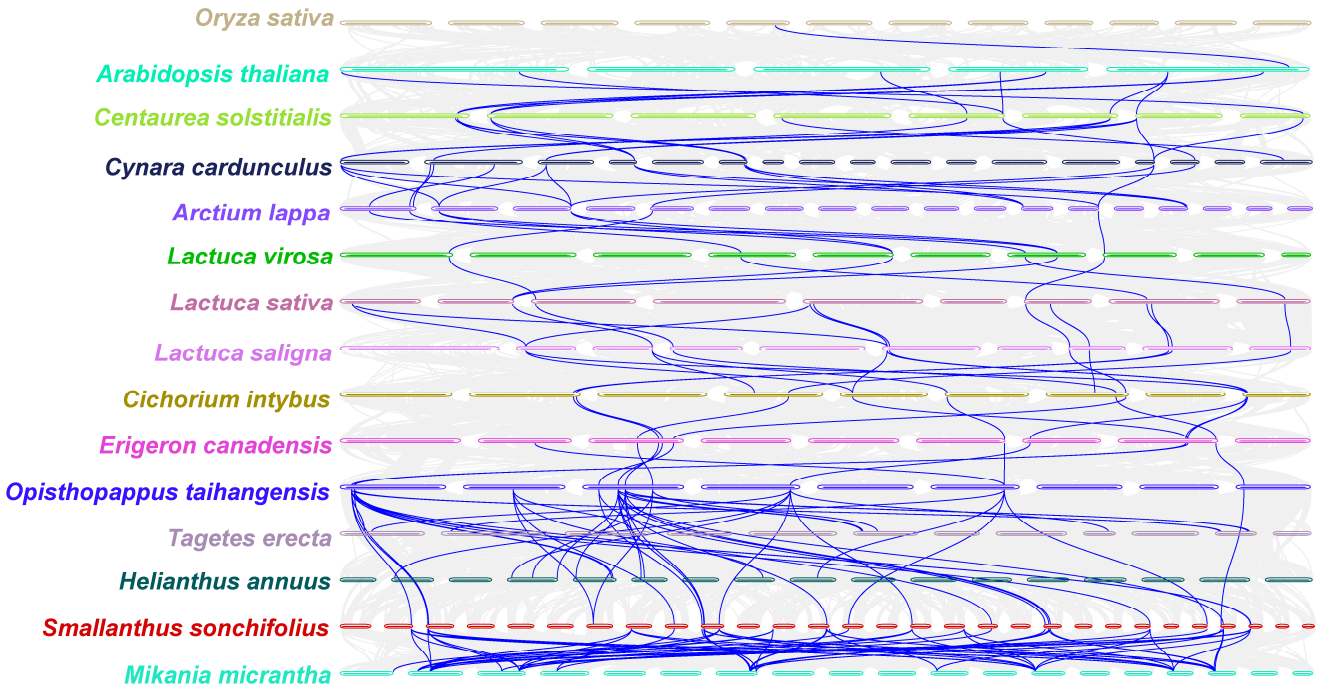


Figure S1: The collinearity analysis between *A. thaliana, O. sativa* and 13 Asteraceae species. Blue lines represented the orthologous *FROs*/*NOXs* gene pairs among these speices

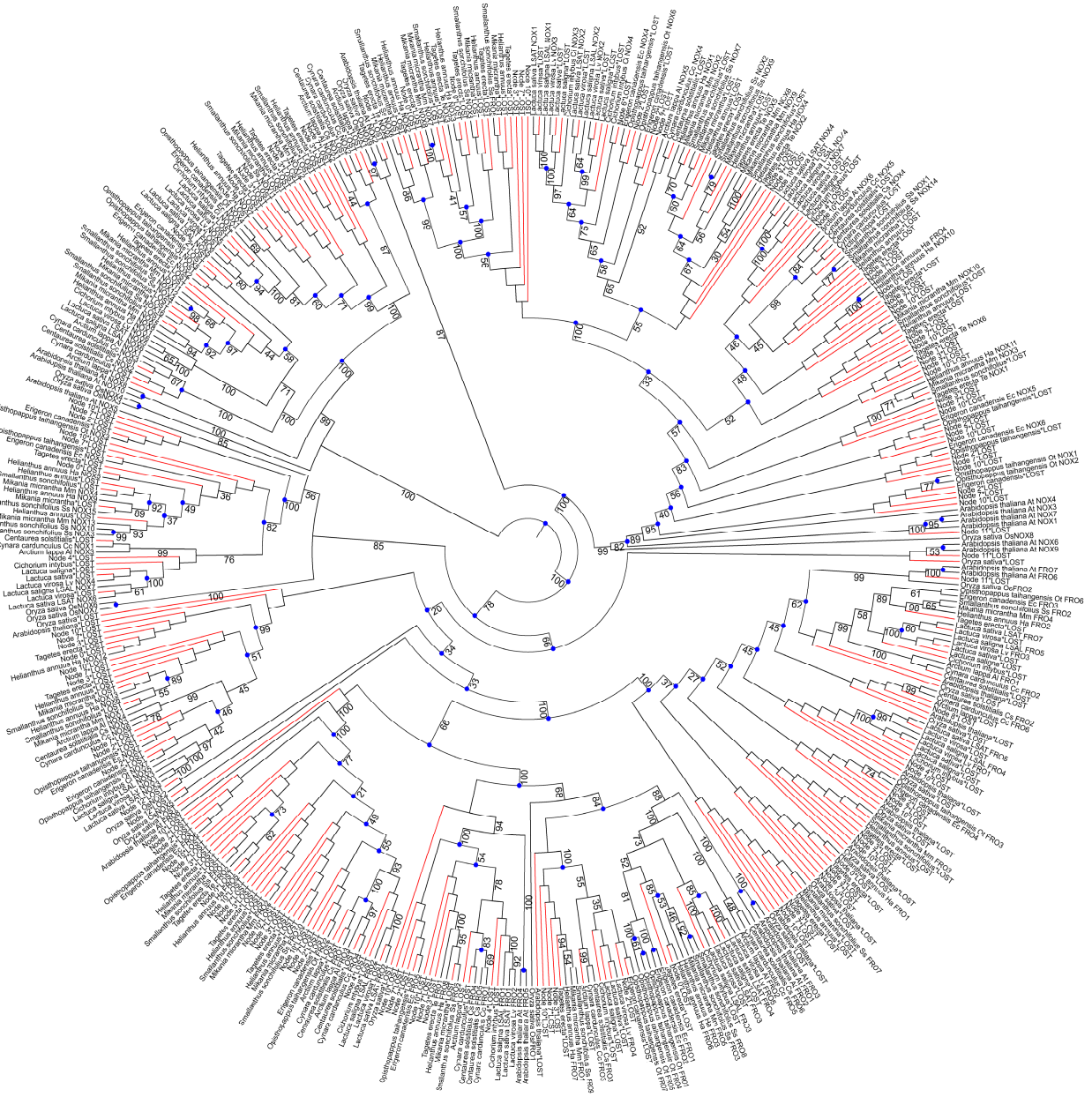


Figure S2: The reconstruction of the gene tree to show the gene gain and lost of *FROs*/*NOXs* in Asteraceae. The nodes marked by blue color indicating gene gain while the branches marked by red indicating gene loss. The number around the nodes represented bootstrap value with1000 times replications

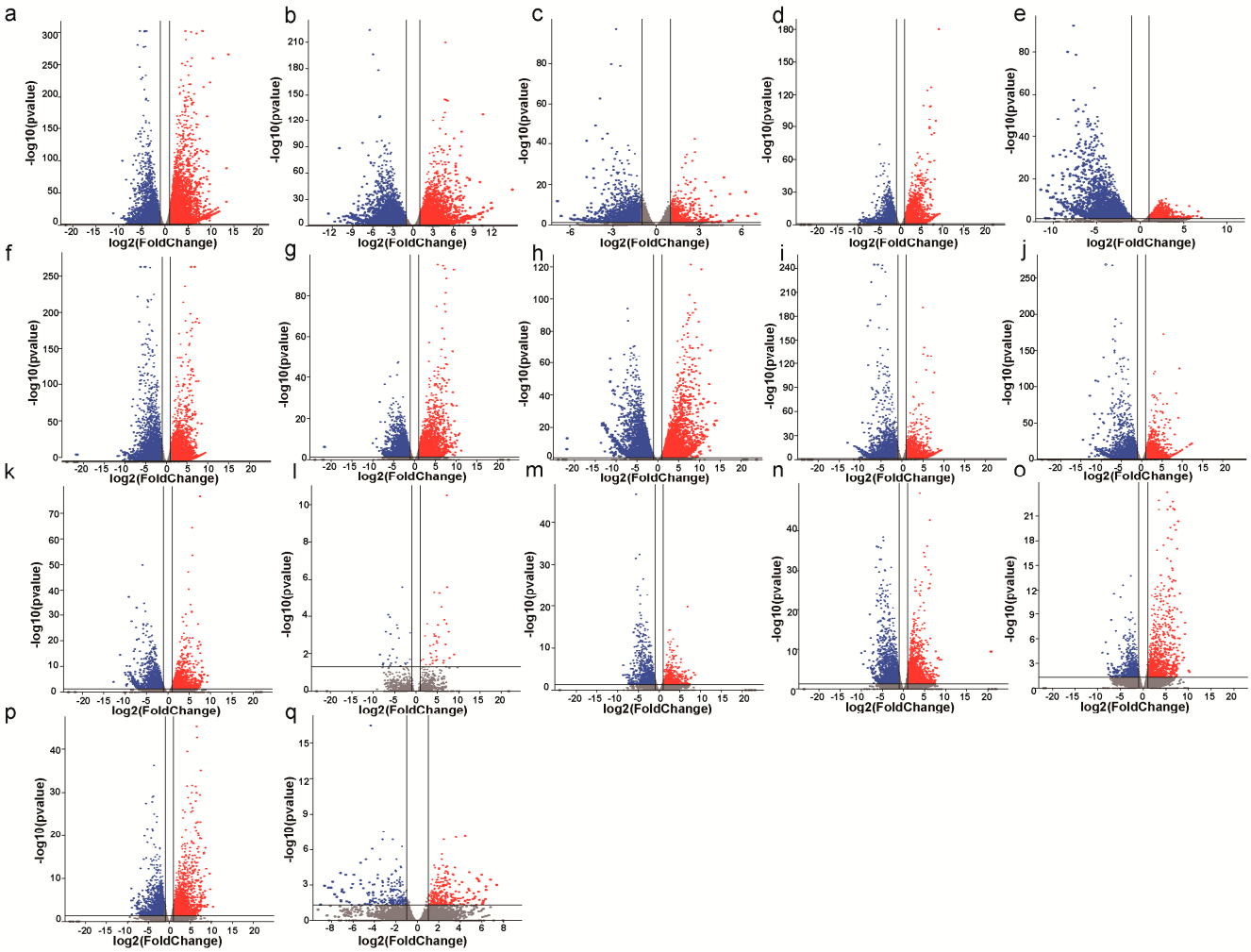


Figure S3: The transcriptome differentially express analysis of (a) L-3.5h vs L-0h, (b) R-9h vs R-0h, (c) H vs CK, (d) L vs CK, (e) H vs L, (f) T_6h vs T_0h, (g) T_24h vs T_0h, (h) T_28h vs T_0h, (i) T_24h vs T_6h, (j) T_48h vs T_6h, (k) T_48h vs T_24h, (l) T_100 vs T_CK, (m) T_300 vs T_CK, (n) T_500 vs T_CK, (o) T_300 vs T_100, (p) T_500 vs T_100 and (q) T_500 vs T_300

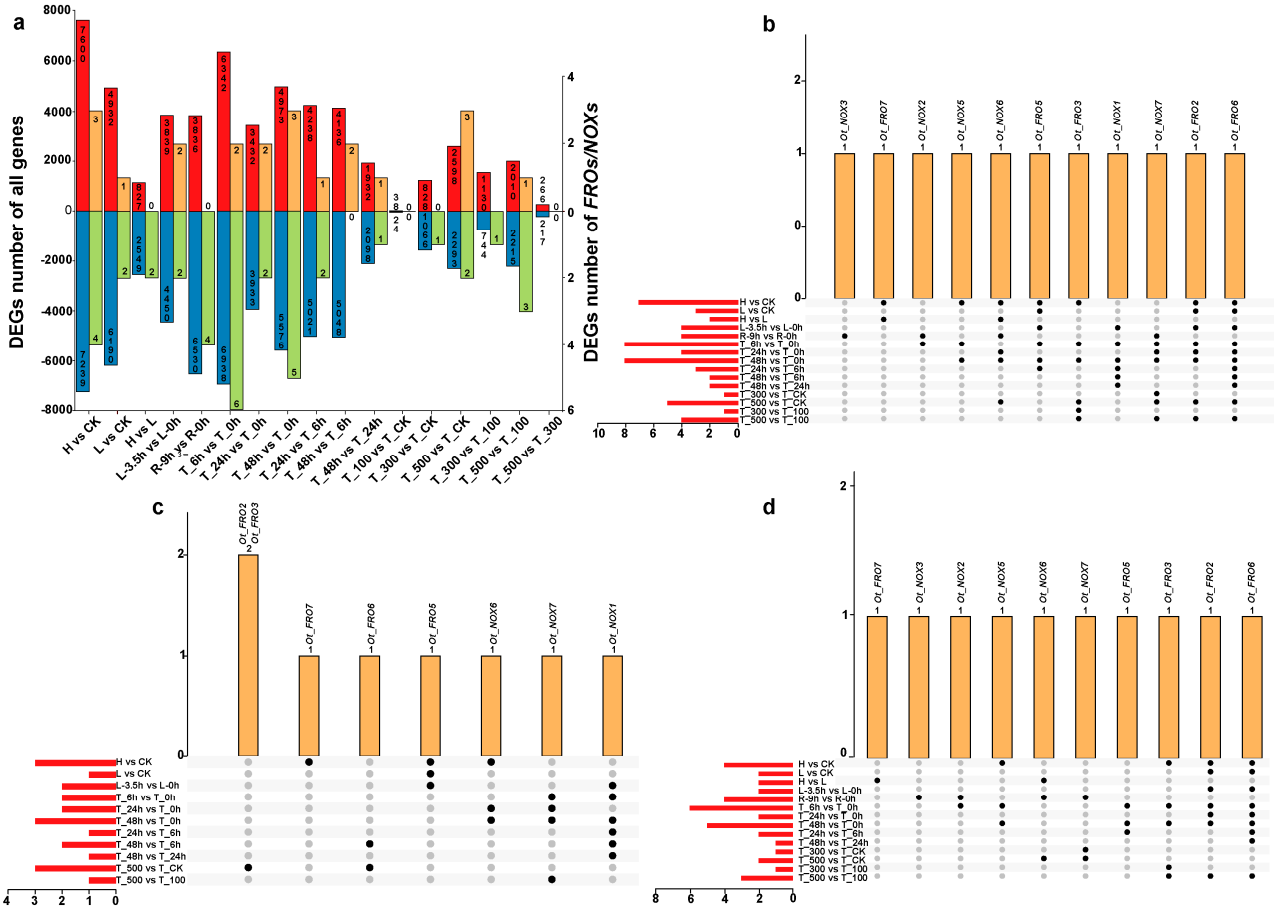


Figure S4: The summary of *FROS/NOXS* expression in *O. taihangensis*. (a) The number of differently expressed genes (DEGs) in whole transcriptome and *FROs/NOXs*, respectively. The UpSet plot of (b) all differently expressed *FROs/NOXs*, (c) upregulated and (d) downregulated members in different compassion, respectively.